

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:34:34 ; Search time 23.63 Seconds

(without alignments)
310.227 Million cell updates/sec

Title: US-09-653-755A-5

Perfect score: 1121

Sequence: 1 ENVLTQSPRIMASPGKVT.....EATHTKTSPIYKSNRNC 214

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	50.1	106	1 KAC_MOUSE	P01837 mus musculu
2	484	43.2	106	1 KACA_RAT	P01836 rattus norv
3	469	41.8	106	1 KACB_RAT	P01835 rattus norv
4	461.5	41.2	129	1 KVAA_MOUSE	P01680 mus musculu
5	430.5	38.4	107	1 KV6F_MOUSE	P04940 mus musculu
6	425.5	38.0	107	1 KV6I_MOUSE	P04943 mus musculu
7	424.5	37.9	107	1 KV6H_MOUSE	P04942 mus musculu
8	421.5	37.6	107	1 KV6G_MOUSE	P04944 mus musculu
9	420.5	37.5	107	1 KV6J_MOUSE	P01675 mus musculu
10	411.5	36.7	107	1 KV6A_MOUSE	P01675 mus musculu
11	411.5	36.7	107	1 KV6D_MOUSE	P01675 mus musculu
12	407.5	36.4	108	1 KV6K_MOUSE	P04945 mus musculu
13	405.5	36.2	107	1 KV6B_MOUSE	P01675 mus musculu
14	403.5	36.0	107	1 KV6C_MOUSE	P01677 mus musculu
15	396.5	35.4	107	1 KV6E_MOUSE	P01679 mus musculu
16	363.5	32.4	129	1 KV3I_MOUSE	P01835 mus musculu
17	360.5	32.2	109	1 KV3E_MOUSE	P01623 mus musculu
18	360.5	32.2	109	1 KV3F_MOUSE	P01624 mus musculu
19	353	31.5	106	1 KAC_MOUSE	P01834 mus musculu
20	352.5	31.4	109	1 KV3B_MOUSE	P01620 mus musculu
21	352.5	31.4	129	1 KV3M_MOUSE	P01835 mus musculu
22	351	31.3	111	1 KV3R_MOUSE	P01670 mus musculu
23	349.5	31.2	109	1 KV3D_MOUSE	P01622 mus musculu
24	345	30.8	111	1 KV3J_MOUSE	P01662 mus musculu
25	344	30.7	129	1 KV1W_MOUSE	P04431 mus musculu
26	344	30.7	131	1 KV3I_MOUSE	P01661 mus musculu
27	343.5	30.6	107	1 KV1D_MOUSE	P01556 mus musculu
28	342	30.5	111	1 KV3H_MOUSE	P01660 mus musculu
29	340	30.5	111	1 KV3T_MOUSE	P01672 mus musculu
30	339.5	30.3	129	1 KV3H_MOUSE	P04207 mus musculu
31	338	30.2	108	1 KV5M_MOUSE	P01646 mus musculu
32	337	30.1	108	1 KV5O_MOUSE	P01648 mus musculu
33	337	30.1	111	1 KV3K_MOUSE	P01663 mus musculu

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
1	KAC_MOUSE	562	50.1	106	1 KAC_MOUSE	P01837 mus musculu
2	KAC_MOUSE	484	43.2	106	1 KACA_RAT	P01836 rattus norv
3	KAC_MOUSE	469	41.8	106	1 KACB_RAT	P01835 rattus norv
4	KAC_MOUSE	461.5	41.2	129	1 KVAA_MOUSE	P01680 mus musculu
5	KAC_MOUSE	430.5	38.4	107	1 KV6F_MOUSE	P04940 mus musculu
6	KAC_MOUSE	425.5	38.0	107	1 KV6I_MOUSE	P04943 mus musculu
7	KAC_MOUSE	424.5	37.9	107	1 KV6H_MOUSE	P04942 mus musculu
8	KAC_MOUSE	421.5	37.6	107	1 KV6G_MOUSE	P04944 mus musculu
9	KAC_MOUSE	420.5	37.5	107	1 KV6J_MOUSE	P01675 mus musculu
10	KAC_MOUSE	411.5	36.7	107	1 KV6A_MOUSE	P01675 mus musculu
11	KAC_MOUSE	411.5	36.7	107	1 KV6D_MOUSE	P01675 mus musculu
12	KAC_MOUSE	407.5	36.4	108	1 KV6K_MOUSE	P04945 mus musculu
13	KAC_MOUSE	405.5	36.2	107	1 KV6B_MOUSE	P01675 mus musculu
14	KAC_MOUSE	403.5	36.0	107	1 KV6C_MOUSE	P01677 mus musculu
15	KAC_MOUSE	396.5	35.4	107	1 KV6E_MOUSE	P01679 mus musculu
16	KAC_MOUSE	363.5	32.4	129	1 KV3I_MOUSE	P01835 mus musculu
17	KAC_MOUSE	360.5	32.2	109	1 KV3E_MOUSE	P01623 mus musculu
18	KAC_MOUSE	360.5	32.2	109	1 KV3F_MOUSE	P01624 mus musculu
19	KAC_MOUSE	353	31.5	106	1 KAC_MOUSE	P01834 mus musculu
20	KAC_MOUSE	352.5	31.4	109	1 KV3B_MOUSE	P01620 mus musculu
21	KAC_MOUSE	352.5	31.4	129	1 KV3M_MOUSE	P01835 mus musculu
22	KAC_MOUSE	351	31.3	111	1 KV3R_MOUSE	P01670 mus musculu
23	KAC_MOUSE	349.5	31.2	109	1 KV3D_MOUSE	P01622 mus musculu
24	KAC_MOUSE	345	30.8	111	1 KV3J_MOUSE	P01662 mus musculu
25	KAC_MOUSE	344	30.7	129	1 KV1W_MOUSE	P04431 mus musculu
26	KAC_MOUSE	344	30.7	131	1 KV3I_MOUSE	P01661 mus musculu
27	KAC_MOUSE	343.5	30.6	107	1 KV1D_MOUSE	P01556 mus musculu
28	KAC_MOUSE	342	30.5	111	1 KV3H_MOUSE	P01660 mus musculu
29	KAC_MOUSE	340	30.5	111	1 KV3T_MOUSE	P01672 mus musculu
30	KAC_MOUSE	339.5	30.3	129	1 KV3H_MOUSE	P04207 mus musculu
31	KAC_MOUSE	338	30.2	108	1 KV5M_MOUSE	P01646 mus musculu
32	KAC_MOUSE	337	30.1	108	1 KV5O_MOUSE	P01648 mus musculu
33	KAC_MOUSE	337	30.1	111	1 KV3K_MOUSE	P01663 mus musculu

RA de Waele P., Feys V., van de Voerde A., Molemans F., Fiers W.;
 RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
 RT directed against the tumour marker human placental alkaline
 RT phosphatase";
 RL Eur. J. Biochem. 176:287-295(1988).

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CC EMBL: V00807; CAA24189.1; -
 CC
 CC PIR: A02119; KIMS.
 CC PIR: S01320; S01320.
 CC InterPro: IPR000495; -
 CC InterPro: IPR003006; -
 CC Pfam: PF00047; 1g; 1.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106
 FT SEQUENCE 106 AA; 11778 MW; 4B51F5EFA9BAEB5 CRC64;

Query Match 50.1%; Score 562; DB 1; Length 106;
 Best Local Similarity 99.1%; Pred. No. 1e-37;
 Matches 105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 109 ADAAPVTSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 168
 DB 1 ADAAPVTSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 60
 OY 169 KSTYSMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 214
 DB 61 KSTYSMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 106

RESULT 2

KACA_RAT
 ID KACA_RAT STANDARD; PRT; 106 AA.
 AC P01836;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG KAPPA CHAIN C REGION, A ALLELE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RX MEDLINE=82082587; PubMed=6273908;
 RA Sheppard H.W., Gutman G.A.;
 RT "Allelic forms of rat kappa chain genes: evidence for strong
 RT selection at the level of nucleotide sequence";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
 DR InterPro: IPR000495; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 1g; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106
 FT SEQUENCE 106 AA; 11732 MW; B7E120D9700DD66 CRC64;

Query Match 43.2%; Score 484; DB 1; Length 106;
 Best Local Similarity 84.9%; Pred. No. 1.3e-31;
 Matches 90; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

OY 109 ADAAPVTSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 168
 DB 1 ADAAPVTSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 60
 OY 169 KSTYSMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 214
 DB 61 KSTYSMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 106

RESULT 3

KACA_RAT
 ID KACA_RAT STANDARD; PRT; 106 AA.
 AC P01835;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG KAPPA CHAIN C REGION, B ALLELE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LOU;
 RX MEDLINE=82082587; PubMed=6273908;
 RA Sheppard H.W., Gutman G.A.;
 RT "Allelic forms of rat kappa chain genes: evidence for strong
 RT selection at the level of nucleotide sequence";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
 RN [2]
 RP SEQUENCE (BENCE-JONES PROTEIN S211).
 RX MEDLINE=75212238; PubMed=807630;
 RA Starace V., Querlin Jean P.;
 RT "The primary structure of a rat kappa Bence Jones protein:
 RT phylogenetic relationships of V- and C-region genes";
 RL J. Immunol. 115:59-62(1975).
 DR PIR: A02117; KIRTB.
 DR InterPro: IPR000495; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 1g; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106
 FT CONFLICT 2 2 D -> N (IN REF. 2).
 FT CONFLICT 30 30 N -> K (IN REF. 2).
 FT CONFLICT 48 48 MISSING (IN REF. 2).
 FT CONFLICT 79 79 E -> Q (IN REF. 2).
 FT CONFLICT 87 87 E -> Q (IN REF. 2).
 FT CONFLICT 98 98 V -> VV (IN REF. 2).
 FT CONFLICT 100 100 S -> N (IN REF. 2).
 FT SEQUENCE 106 AA; 11601 MW; 4CFA7CA820D1CA36 CRC64;

Query Match 41.8%; Score 469; DB 1; Length 106;
 Best Local Similarity 81.1%; Pred. No. 1.9e-30;
 Matches 86; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

OY 109 ADAAPVTSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 168
 DB 1 ADAAPVTSIFPPSSSEQLTSGGASVCFLNFPYPRDINVKWKIDGSRONGVLSMTDQDS 60
 OY 169 KSTYSMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 214
 DB 61 KSTYSMSSTLTITKDEYERHNSYTCGATHTKSTSPYKSFNNEC 106

RESULT 4

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KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT: 129 AA.
AC P01680:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION S107B PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107."
RL Cell 26:57-66(1981).
CC -I- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
-----
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-----
DR EMBL: J00577; AAA38780.1; -
DR EMBL: V00780; CAA24157.1; -
DR PIR: A01943; KXMS7B.
DR HSSP: P01679; ZFBJ.
DR InterPro: IPR003006; -
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 58 72 FRAMEWORK 2.
FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 80 111 FRAMEWORK 3.
FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 128 FRAMEWORK 4.
FT DISULFID 45 111 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13833 MW; EABB73072DC6B64 CRC64;
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Query Match 41.2%; Score 461.5; DB 1; Length 129;
Best Local Similarity 87.0%; Pred. No. 9.4e-30;
Matches 94; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=832271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification."
RL Nature 304:320-324(1983).
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
-----
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-----
DR EMBL: K00735; AAA36680.1; -
DR InterPro: IPR003006; -
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 34 48 FRAMEWORK 2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 56 87 FRAMEWORK 3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 97 106 FRAMEWORK 4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68B6 CRC64;
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Query Match 38.4%; Score 430.5; DB 1; Length 107;
Best Local Similarity 80.4%; Pred. No. 2e-27;
Matches 86; Conservative 8; Mismatches 10; Indels 3; Gaps 2;

```


OX	NCHI_TaxID=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=79082830; PubMed=103573;
RA	Rao D.N., Rudikoff S., Potter M.;
RT	"Kappa Chain variable regions from three galactan binding myeloma proteins.";
RL	Biochemistry 17:5555-5559(1978).
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
DR	PIR: A01941; KMSX4.
DR	HSSP: P01679; 2FBJ.
DR	InterPro: IPR003006; -.
KW	Pfam; PF00047; 1g; 1.
FT	Immunoglobulin V region.
FT	DOMAIN 1 23 FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 2 34 48 FRAMEWORK 2. FRAMEWORK 2.
FT	DOMAIN 3 49 55 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 4 56 87 FRAMEWORK 3. FRAMEWORK 3.
FT	DOMAIN 5 88 96 COMPLEMENTARITY-DETERMINING 3.
FT	DISULFD 97 106 FRAMEWORK 4. FRAMEWORK 4.
FT	NON_TER 107 107 BY SIMILARITY.
SO	SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;
Query Match	36.7%; Score 411.5; DB 1; Length 107;
Best Local Similarity	78.0%; Pred. No. 6,1e-26;
Matches 85; Conservative	8; Mismatches 13; Indels 3; Gaps 2;
OY	1 ENVLTSFPAIMASAFGEKVMTGRASSVSSSLHYHWRQSGASPKLMIYSTSNLISGVP 60 : : : : : : : : : : : : : : :
DB	1 EIVLTQSFAITTAASLGQKVTITCSASSV--SYMHMYOQKSGTSPKPWIETSKLASGV 58 : : : : : : : : : : : : : : :
OY	61 ARFSGGSGSTSYSLTISSVEADATYYCQOXS-GYRFEGGTKEIKR 108 : : : : : : : : : : : : : : :
DB	59 ARFSGGSGSTSYSLTISSMEADAIYYCOQNMYPLMTFGGGTKEIKR 107 : : : : : : : : : : : : : : :
RESULT 11	
KV6D_MOUSE	STANDARD; PRT; 107 AA.
ID KV6D_MOUSE	P01678;
AC	21-JUL-1986 (Rel. 01, Created)
DJ	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, last annotation update)
DE	IG KAPPA CHAIN V-VI REGION SAPC 10.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCHI_TaxID=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=81054757; PubMed=6776525;
RA	Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT	"Kappa Chain joining segments and structural diversity of antibody combining sites.";
RL	Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
DR	PIR: A01941; KMSX4.
DR	HSSP: P01679; 2FBJ.
DR	InterPro: IPR003006; -.
KW	Pfam; PF00047; 1g; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23 FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 2 34 48 FRAMEWORK 2. FRAMEWORK 2.
FT	DOMAIN 3 49 55 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 4 56 87 FRAMEWORK 3. FRAMEWORK 3.
FT	DOMAIN 5 88 96 COMPLEMENTARITY-DETERMINING 3.
FT	DISULFD 97 106 FRAMEWORK 4. FRAMEWORK 4.
FT	NON_TER 107 107 BY SIMILARITY.
SO	SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;

FT DISULFID 23 87 BY SIMILARITY.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA: 11554 MW: 27A2D022A5EC34D7 CRC64;

Query Match 36.7%; Score 411.5; DB 1; Length 107;
 Best Local Similarity 78.0%; Pred. No. 6.1e-26;
 Matches 85; Conservative 8; Mismatches 13; Indels 3; Gaps 2;

OY 1 ENVLQSPAIMSAPGEKVTMTGRASSVSSSYLHWYRQKSGAPKMTYSTNLASGVP 60
 1 EYLQSPAITASLGQKVTITCSASSV--SYMHWYQOKSGSPKPMYELISKLASGVP 58

OY 61 ARPSGSGSTSYSLTSSVEADATYTCQOYS-GYRFGGKLEIKR 108
 DB 59 ARPSGSGSTSYSLTSSMEADATYTCQOWNYPLTFGGKLEIKR 107

RESULT 12

KV6C_MOUSE STANDARD; PRT; 108 AA.
 AC P04945;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-VI REGION NQ2-6.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=83271467; PubMed=6877353;
 RA Kaathinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-
 RT phenylloxazalone and its early diversification".
 RL Nature 304:320-324(1983).

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CC EMBL: K00746; AAA38691.1; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Ig. 1.
 DR Immunoglobulin V region; Hybridoma.
 KM DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 1 24 33 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 34 48 FRAMEWORK 2.
 FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 56 87 FRAMEWORK 3.
 FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 99 108 FRAMEWORK 4.
 FT DISULFID 23 87 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA: 11713 MW: DABF235CD9680AC6 CRC64;

Query Match 36.4%; Score 407.5; DB 1; Length 108;
 Best Local Similarity 75.0%; Pred. No. 1.3e-25;
 Matches 81; Conservative 12; Mismatches 10; Indels 5; Gaps 2;

OY 3 VLTQSPAIMSAPGEKVTMTGRASSVSSSYLHWYRQKSGAPKMTYSTNLASGVP 62
 3 LVTQSPAIMSAPGKVTMTGRASSV--SYMHWYQOKSGSPRLITYDTSNLASGVP 60

OY 63 FSGSGSTSYSLTSSVEADATYTCQOYSG---RTFGGKLEIKR 107
 DB 61 FSGSGSTSYSLTTRMQAEDATYTCQOWSSYPPMLTFGAGTKLEIK 108

RESULT 13
 KV6C_MOUSE STANDARD; PRT; 107 AA.

AC P01676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-VI REGION XRPC 24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE.
 RA MEDLINE=79082830; PubMed=103573;
 RA Rao D.N., Rudikoff S., Potter M.;
 RT "k Chain variable regions from three galactan binding myeloma
 RT proteins".
 RL Biochemistry 17:5555-5559(1978).
 CC -I MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BIND GALACTAN

DR PIR: A01941; KVMX4.
 DR HSSP: P01679; 2F8J.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Ig. 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 34 48 FRAMEWORK 2.
 FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 56 87 FRAMEWORK 3.
 FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 97 106 FRAMEWORK 4.
 FT DISULFID 23 87 BY SIMILARITY.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA: 11584 MW: 36E6D022A5EC34D7 CRC64;

Query Match 36.2%; Score 405.5; DB 1; Length 107;
 Best Local Similarity 77.1%; Pred. No. 1.8e-25;
 Matches 84; Conservative 8; Mismatches 14; Indels 3; Gaps 2;

OY 1 ENVLQSPAIMSAPGEKVTMTGRASSVSSSYLHWYRQKSGAPKMTYSTNLASGVP 60
 1 EYLQSPAITASLGQKVTITCSASSV--SYMHWYQOKSGSPKPMYELISKLASGVP 58

OY 61 ARPSGSGSTSYSLTSSVEADATYTCQOYS-GYRFGGKLEIKR 108
 DB 59 ARPSGSGSTSYSLTSSMEADATYTCQOWNYPLTFGGKLEIKR 107

RESULT 14

KV6C_MOUSE STANDARD; PRT; 107 AA.

AC P01677;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-VI REGION TEPC 60I/TEPC 19I.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE (TEPC 60I).
 RA MEDLINE=79082830; PubMed=103573;
 RA Rao D.N., Rudikoff S., Potter M.;
 RT "k Chain variable regions from three galactan binding myeloma
 RT proteins".
 RL Biochemistry 17:5555-5559(1978).
 RN [2]

